```
        FILE 'MEDLINE' ENTERED AT 14:38:55 ON 06 AUG 2007
L1      178942 S (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L2         810 S L1 AND (VPR OR VIRAL PROTEIN R)
L3           8 S L2 AND (MONOCLONAL ANTIBOD?)
L4          83 S L2 AND ANTIBOD?
L5          75 S L4 NOT L3
L6           6 S L5 AND ANTI-VPR

        FILE 'BIOSIS' ENTERED AT 14:43:34 ON 06 AUG 2007
L7      172040 S (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L8         923 S L7 AND (VPR OR VIRAL PROTEIN R)
L9          58 S L8 AND ANTIBOD?
L10          8 S L9 AND MONOCLONAL
L11         50 S L9 NOT L10

=> log off
```
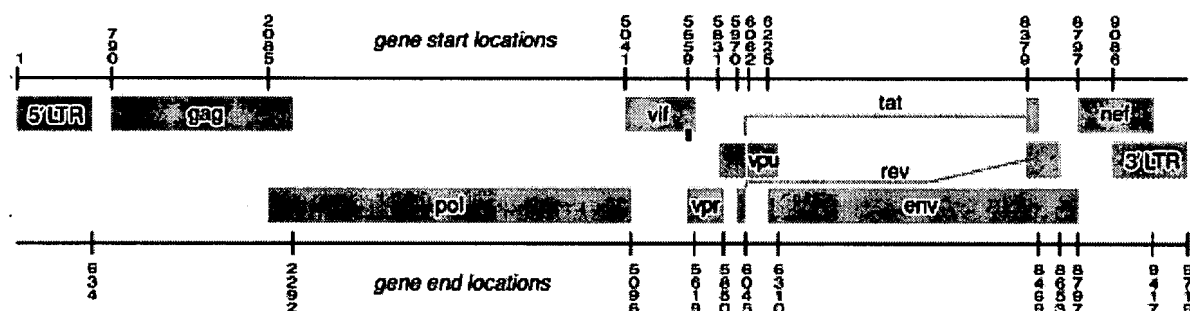
Vpr Ab Epitope Map

The names of MAbs and the location of well characterized linear binding sites of 21 amino acids or less are indicated relative to the protein sequences of the HXB2 clone. This map is meant to provide the relative location of epitopes on a given protein, but the HXB2 sequence may not actually bind to the MAb of interest, as it may vary relative to the sequence for which the epitope was defined. Above each linear binding site, the MAb name is given followed by the species in parentheses. Human is represented by `h', non-human primate by `p', mouse by `m', and others by `o'. More precise species designations for any given MAb can be found using the web search interface.

```
MEQAPEDQGPQREPHNEWTLELLEELKNEAVRHFPRIWLHGLGQHIYETY
         |         |         |         |         |
        10        20        30        40        50
GDTWAGVEAIIRILQQLLFIHFRIGCRHSRIGVTRQRRARNGASRS
         |         |         |         |
        60        70        80        90
```

Last modified: Wed Apr 11 14:48:25 2007

Query location shown as red bar in map between reading frames 1 and 2.

Query: seq1   EQAPEDQGPQR

Query Length: 11

HXB2 Location: genome: 5562→5594 protein: Vpr 2→12

Alignment used: HIV1VprPRO, 910 sequences

| Summarize All | Summarize By Subtype | Find Other Matches |

| Download | alignment below in format | table / fasta / mase / pretty |

"-" = identity to query sequence
"." = gap in sequence
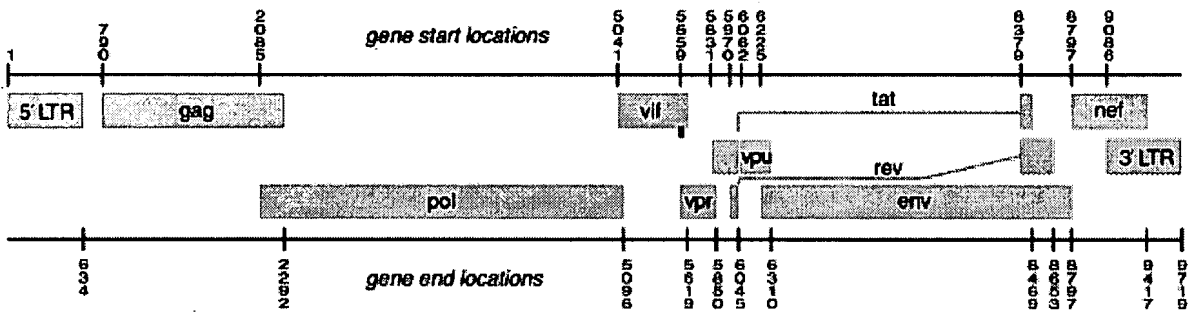"RED" = perfect identity to query sequence

```
                        seq1 EQAPEDQGPQ R
         B.FR.83.HXB2_K03455 ---------- -
       A.SN.01.DDI579_AY521629 ---------- -
       A.SN.01.DDJ369_AY521631 ---------- -
       A.SN.96.DDJ360_AY521630 ---------- -
      A.UA.x.98UA0116_AF413973 ---------- -
      A.UA.x.98UA0116_AF413974 ---------- -
      A.UA.x.98UA0116_AF413975 ---------- -
      A.UA.x.98UA0116_AF413976 ---------- -
     A1.KE.00.KER2008_AF457052 ---------- -
     A1.KE.00.KER2009_AF457053 ---------- -
     A1.KE.00.KER2012_AF457055 ---------- -
     A1.KE.00.KNH1144_AF457066 ---------- -
     A1.KE.00.KNH1199_AF457067 ---------- -
     A1.KE.00.KNH1207_AF457068 -R-------- -
```

```
A1.KE.00.KNH1209_AF457069 ----------  -
A1.KE.00.KNH1211_AF457070 --T-------  -
A1.KE.00.KNH1214_AF457071 ----------  K
A1.KE.00.KSM4024_AF457077 ----------  -
A1.KE.00.KSM4030_AF457079 ---------P  -
A1.KE.00.MSA4069_AF457080 ----------  -
A1.KE.00.MSA4070_AF457081 ----------  -
A1.KE.00.MSA4072_AF457083 ----------  -
A1.KE.00.MSA4076_AF457084 ----------  -
A1.KE.00.MSA4079_AF457086 ----------  -
A1.KE.00.NKU3005_AF457089 ----------  -
A1.KE.00.NKU3007_AF457091 ----------  -
A1.KE.86.ML013_10_AY322184 ----------  -
```

QuickAlign   <u>Help</u>

Query location shown as red bar in map between reading frames 1 and 2.

Query: seq1   `CEQAPEDQGPQ`

Query Length: 11

<u>HXB2 Location:</u>   genome: 5559→5591 protein: Vpr 1→11

<u>Alignment used:</u>   HIV1VprPRO, 910 sequences

[Summarize All]   [Summarize By Subtype]   [Find Other Matches]

[Download]   alignment below in format

table	▲
fasta	▬
mase	
pretty	▼

"-" = identity to query sequence
"." = gap in sequence
"RED" = perfect identity to query sequence

```
                         seq1 CEQAPEDQGP Q
            B.FR.83.HXB2_K03455 M--------- -
          A.SN.01.DDI579_AY521629 M--------- -
          A.SN.01.DDJ369_AY521631 M--------- -
          A.SN.96.DDJ360_AY521630 M--------- -
         A.UA.x.98UA0116_AF413973 M--------- -
         A.UA.x.98UA0116_AF413974 M--------- -
         A.UA.x.98UA0116_AF413975 M--------- -
         A.UA.x.98UA0116_AF413976 M--------- -
        A1.KE.00.KER2008_AF457052 M--------- -
        A1.KE.00.KER2009_AF457053 M--------- -
        A1.KE.00.KER2012_AF457055 M--------- -
        A1.KE.00.KNH1144_AF457066 M--------- -
        A1.KE.00.KNH1199_AF457067 M--------- -
        A1.KE.00.KNH1207_AF457068 M-R------- -
```

```
A1.KE.00.KNH1209_AF457069 M---------- -
A1.KE.00.KNH1211_AF457070 M--T------- -
A1.KE.00.KNH1214_AF457071 I---------- -
A1.KE.00.KSM4024_AF457077 M---------- -
A1.KE.00.KSM4030_AF457079 M---------- P
A1.KE.00.MSA4069_AF457080 M---------- -
A1.KE.00.MSA4070_AF457081 M---------- -
A1.KE.00.MSA4072_AF457083 M---------- -
A1.KE.00.MSA4076_AF457084 M---------- -
A1.KE.00.MSA4079_AF457086 M---------- -
A1.KE.00.NKU3005_AF457089 M---------- -
A1.KE.00.NKU3007_AF457091 M---------- -
A1.KE.86.ML013_10_AY322184 M---------- -
```